GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 14:24:06 ; Search time 319 Seconds
(without alignments)
12453.057 Million cell updates/sec

Title: US-09-815-923-3
Perfect score: 1764
Sequence: 1 atgccgccgtcggacgcgcc.....ctaccctatgcaacctgtga 1764

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
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24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	891.2	50.5	2471	23	ABL07643	Drosophila melanog
	2	579.4	32.8	2278	16	AAQ94016	Rat 5HT transporte
	3	579.4	32.8	2415	16	AAQ94017	Rat 5HT transporte
	4	576.2	32.7	2278	14	AAQ41055	Rat 5HT transporte
	5	576	32.7	2415	14	AAQ41056	Rat 5HT transporte
	6	557	31.6	2756	13	AAQ26646	Encodes 5HTT serot
	7	554	31.4	1890	22	AAF73818	Partial human SLC6
	8	552.4	31.3	2508	14	AAQ41057	Human 5HT transpor
	9	552.4	31.3	2508	16	AAQ94018	Human 5HT transpor
	10	552.4	31.3	2889	20	AAX57846	Human serotonin tr
	11	552.4	31.3	2889	22	AAC85219	Human serotonin tr
	12	522.4	29.6	1854	22	AAH28082	Nucleotide sequenc
	13	522.4	29.6	1854	22	AAH28086	Nucleotide sequenc
	14	522.4	29.6	1983	13	AAQ28118	Human norepinepher
	15	520.8	29.5	1854	22	AAH28083	DNA encoding human
	16	520.8	29.5	1854	22	AAH28087	DNA encoding human
	17	504.6	28.6	3919	14	AAQ53413	Sequence of the p
	18	504.6	28.6	3946	24	ABL68342	Kidney cancer rela
	19	484.6	27.5	2640	13	AAQ26664	bDAT. Bos taurus.
	20	464.4	26.3	1985	14	AAQ41172	Dopamine transport
	21	462.8	26.2	3404	13	AAQ26683	Rat dopamine trans
	22	435.6	24.7	2504	22	AAC92096	Cabbage looper OA/
	23	433.6	24.6	2074	23	ABL13989	Drosophila melanog
	24	424	24.0	4317	22	AAH57574	Human brain cell s
	25	422.4	23.9	2863	22	ABA08949	Human GABA transpo
	26	416.2	23.6	1997	24	AAD23977	Human neurotransmi
	27	407.8	23.1	4074	24	ABI99626	Mouse ischaemic co
	28	396.6	22.5	1938	14	AAQ48761	GAT-3 GABA transpo
	29	393.4	22.3	1938	22	AAF85420	Nucleotide sequenc
	30	391.8	22.2	2062	15	AAQ44335	GAT-B transporter
	31	381.2	21.6	1809	24	AAH77167	Human GABA transpo
c	32	379.2	21.5	6723	23	ABL07642	Drosophila melanog
	33	374.2	21.2	2028	22	AAF85419	Nucleotide sequenc
	34	374.2	21.2	2028	24	ABK63522	Rat sequence diffe
	35	374.2	21.2	2283	24	ABL65250	Lung cancer relate
	36	374.2	21.2	2283	24	ABL66320	Lung cancer relate
	37	372.6	21.1	1991	22	AAF85439	Nucleotide sequenc
	38	371	21.0	1991	14	AAQ48764	GAT-3 transporter
	39	369	20.9	1806	22	AAF59518	Human GABA transpo
	40	369	20.9	2168	24	AAD23973	Human neurotransmi
	41	367.8	20.9	2028	14	AAQ48760	GAT-2 GABA transpo
	42	366.4	20.8	2728	18	AAT58853	cDNA encoding high
	43	366.4	20.8	2728	19	AAV28861	Rat proline transp
	44	366.2	20.8	2217	15	AAQ66982	Human betaine-GABA
	45	366.2	20.8	2217	17	AAT16542	Human betaine/GABA

ALIGNMENTS

RESULT 1
ABL07643
ID ABL07643 standard; cDNA; 2471 BP.
XX
AC ABL07643;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17411.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB63540.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more

```
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 17411; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2471 BP; 510 A; 723 C; 690 G; 548 T; 0 other;

  Query Match           50.5%;  Score 891.2;  DB 23;  Length 2471;
  Best Local Similarity  71.7%;  Pred. No. 4.7e-231;
  Matches 1185;  Conservative    0;  Mismatches  458;  Indels    9;  Gaps    1;

Qy         22 CCCGCGCCCACCGCGCCACCTCCTGATCTTCCTGCTACCACCGCTCAGAAAAGCCGTTCG 81
Db        130 CACACGACGCCCGCCAAGGTCACCGATCCACTGGCCCCCAAGCTGGCCAACAACGAGCGC 189

Qy         82 GTGGTGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTC 141
Db        190 ATTCTGGTGGTCTCCGTGACGGAGAGGACTCGCGAGACCTGGGGACAGAAGGCGGAGTTC 249

Qy        142 CTGCTGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATC 201
Db        250 CTCCTGGCCGTGATTGGGTTCGCAGTGGATCTGGGCAATGTGTGGCGCTTCCCGTACATC 309

Qy        202 TGTTACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGC 261
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Qy        262 GGGCTGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTC 321
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Qy        322 ACTCTCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATC 381
Db        430 AGCATCTGGAAGCGCATCTGTCCGGCCCTAAAAGGCGTGGGCTATGCGATCTGCCTAATC 489

          382 GACATCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATC 441
          490 GACATTTATATGGGCATGTACTACAACACGATTATCGGCTGGGCGGTATACTACCTCTTC 549

Qy        442 GCTTCTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAAC 501
Db        550 GCCTCGTTCACATCCA---------AGTTGCCGTGGACGTCGTGCGATAATCCCTGGAAC 600

Qy        502 ACGCCGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCG 561
Db        601 ACTGAGAACTGCATGCAGGTGACCAGTGAGAACTTCACGGAACTGGCCACGTCGCCGGCC 660

Qy        562 AAGGAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATG 621
Db        661 AAGGAGTTCTTTGAGCGAAAGGTTTTGGAGAGCTACAAGGGCAACGGGCTGGACTTCATG 720

Qy        622 GGGCCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTC 681
Db        721 GGTCCGGTGAAGCCCACGCTGGCACTCTGCGTCTTCGGGGTCTTTGTCCTGGTCTACTTC 780

Qy        682 TCCTTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCG 741
Db        781 TCCCTGTGGAAGGGAGTGCGCAGTGCCGGAAAGGTGGTGTGGGTCACCGCTCTGGCTCCT 840

Qy        742 TACGTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGC 801
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Qy        802 ATACGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGAC 861
Db        901 ATCAAGTACTACCTAACCCCGGAGTGGCACAAACTGAAGAACTCCAAAGTCTGGATCGAC 960

Qy        862 GCGGCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCC 921
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Qy        922 AGCTACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAAC 981
Db       1021 AGCTACAACAAGTTCAACAACAACTGCTATCGCGATGCTCTCATCACCAGCAGCATCAAC 1080

Qy        982 TGCTTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCAC 1041
Db       1081 TGCTTGACCAGTTTCCTGGCCGGCTTTGTCATCTTCTCCGTTTTGGGGTACATGGCCTAC 1140

Qy       1042 GTTCAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTG 1101
Db       1141 GTCCAAAAGACCTCCATCGACAAGGTGGGCCTGGAGGGTCCGGGGCTGGTGTTCATCGTT 1200

Qy       1102 TACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTC 1161
Db       1201 TACCCGGAGGCCATAGCCACGATGAGTGGCTCGGTGTTCTGGAGCATCATCTTCTTCCTG 1260

Qy       1162 ATGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCT 1221
Db       1261 ATGCTGATTACCCTGGGACTGGACAGCACCTTTGGCGGATTGGAGGCGATGATAACAGCG 1320

Qy       1222 CTTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTG 1281
Db       1321 CTGTGCGACGAGTATCCGCGAGTGATTGGCAGGCGCAGGGAGCTGTTCGTCCTGCTGCTC 1380

Qy       1282 CTTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTA 1341
Db       1381 CTGGCTTTCATCTTCCTGTGCGCCCTTCCCACGATGACCTACGGTGGCGTGGTGCTGGTC 1440

Qy       1342 GACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCT 1401
Db       1441 AACTTCCTGAATGTCTACGGACCCGGGTTGGCCATCCTCTTTGTGGTCTTCGTGGAGGCA 1500

Qy       1402 GCCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTG 1461
Db       1501 GCCGGAGTCTTTTGGTTCTACGGAGTGGACCGCTTCAGCTCGGATGTGGAACAGATGCTG 1560

Qy       1462 GGGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTG 1521
Db       1561 GGCAGCAAGCCAGGCTTATTCTGGCGGATCTGCTGGACGTACATCAGCCCTGTGTTCCTG 1620

Qy       1522 CTGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACC 1581
Db       1621 CTGACCATATTCATTTTCTCCATCATGGGCTACAAGGAGATGCTCGGCGAGGAGTACTAC 1680

Qy       1582 TATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATT 1641
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Qy       1642 CCTCTTTACATTATCTACAAACTGCTCATCAC 1673
Db       1741 CCCATGTACATTATCTACAAGTTCTTCTTCGC 1772


RESULT 2
AAQ94016
ID   AAQ94016 standard; cDNA; 2278 BP.
XX
AC   AAQ94016;
XX
DT   02-DEC-1995  (first entry)
XX
DE   Rat 5HT transporter (rSERT) encoded by BS4E-10.
XX
```

KW Serotonin transporter; 5-hydroxytryptamine; 5HT; noradrenaline; NA;
KW SERT; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 48..1868
FT /*tag= a
XX
PN US5418162-A.
XX
PD 23-MAY-1995.
XX
PF 22-OCT-1991; 91US-0778231.
XX
PR 14-OCT-1992; 92US-0959943.
PR 22-OCT-1991; 91US-0778231.
XX
PA (UYDU-) UNIV DUKE.
PA (UYEM-) UNIV EMORY.
XX
Blakely RD, Caron MG, Fremeau RT;
XX
DR WPI; 1995-199742/26.
DR P-PSDB; AAR76072.
XX
PT DNA encoding rat serotonin transporter - useful in the rational design of
PT drugs and for screening for RFLP associated with certain disorders
XX
PS Claim 1; column 21-26; 27pp; English.
XX
CC An isolated DNA comprising AAQ94016 is claimed. An example describes
CC the isolation of a cDNA encoding the rat 5HT transporter. A
CC synthetic antisense oligo corresp. to the poorly conserved AA
CC sequence in the 5' end of PCR clone rMB6-25 was used to screen a rat
CC brainstem cDNA library by plaque hybridisation. One positive plaque
CC was identified. The insert, designated BS4E-10, was sequenced.
CC Sequences obtd. from two separate, partial cDNAs isolated from a rat
CC midbrain cDNA library in a separate screen were also used to confirm
CC the sequence and interpret compressions. The nt and deduced AA
CC sequence of the rat 5HT transporter (rSERT) encoded by BS4E-10 is
CC given in AAQ94016 and AAR76072 respectively. Sequences from bps 297-
CC 974 match those obtd. from the partial cDNA clone rMB6-25. The ORF
CC predicts a protein with a rel. mol. mass of 68,000 (Mr, 68K) and
CC is distinguished by the presence of 11-12 regions of significantly
CC extended hydrophobicity sutiable for the formation of transmembrane
CC domains. Two potential N-linked glycosylation sites are present on
CC a large hydrophilic domain between putative TM domains 3 and 4. One
CC consensus site for cAMP-dependent protein kinase phosphorylation
CC is present near the end of the NH2-terminus.
XX
SQ Sequence 2278 BP; 501 A; 654 C; 576 G; 547 T; 0 other;

Query Match 32.8%; Score 579.4; DB 16; Length 2278;
Best Local Similarity 60.0%; Pred. No. 1.5e-146;
Matches 983; Conservative 0; Mismatches 651; Indels 3; Gaps 1;

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Qy        86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
Db       187 TGGTGGCTGAGATTCGCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 246

Qy       146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
Db       247 TGTCCGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 306

Qy       206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
Db       307 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 366

Qy       266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
Db       367 TCCCGCTCTTTTACATGGAGCTCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCA 426

Qy       326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
Db       427 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 486

Qy       386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
Db       487 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 546

Qy       446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
Db       547 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 606

Qy       506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
Db       607 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 666

Qy       566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
Db       667 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 726

Qy       626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
Db       727 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 786

Qy       686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
Db       787 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 846

Qy       746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
Db       847 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 906

Qy       806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
Db       907 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 966

Qy       866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
Db       967 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1026

Qy       926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
Db      1027 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1086

Qy       986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
Db      1087 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1146

Qy      1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
Db      1147 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1206

Qy      1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
Db      1207 ATGCAGAGGCAATAGCCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1266

Qy      1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db      1267 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1326

Qy      1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db      1327 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1386

Qy      1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
Db      1387 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1446

Qy      1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
Db      1447 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1506

Qy      1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
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Db       1507 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1566

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522

Db       1567 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1626

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582

Db       1627 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1686

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642

Db       1687 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1746

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702

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         1703 CAATCCAACGTCCGGAA 1719

Db       1807 AAAGTATCACTCCTGAA 1823
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```
RESULT 3
AAQ94017
ID   AAQ94017 standard; cDNA; 2415 BP.
XX
AC   AAQ94017;
XX
DT   02-DEC-1995  (first entry)
XX
DE   Rat 5HT transporter (rSERT) encoded by BS4E-10.
XX
KW   Serotonin transporter; 5-hydroxytryptamine; 5HT; noradrenaline; NA;
KW   SERT; ss.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             116..2005
FT                   /*tag= a
XX
PN   US5418162-A.
XX
PD   23-MAY-1995.
XX
     22-OCT-1991;   91US-0778231.

     14-OCT-1992;   92US-0959943.
PR   22-OCT-1991;   91US-0778231.
XX
PA   (UYDU-) UNIV DUKE.
PA   (UYEM-) UNIV EMORY.
XX
PI   Blakely RD,  Caron MG,  Fremeau RT;
XX
DR   WPI; 1995-199742/26.
DR   P-PSDB; AAR76073.
XX
PT   DNA encoding rat serotonin transporter - useful in the rational design of
PT   drugs and for screening for RFLP associated with certain disorders
XX
PS   Claim 3; column 29-34; 27pp; English.
XX
CC   An isolated DNA comprising AAQ94017 is claimed. This is the result of
CC   further sequencing of rat 5HT transporter cDNA BS4E-10. While the
CC   sequence obtd. in a previous example (see 94016) was essentially
CC   correct, further sequencing refined the knowledge of the actual
CC   sequence of rat 5HT transporter cDNA. Sequences from bases 279-
CC   974 match those obtd. from the partial cDNA clone rMB6-25. The
CC   ORF predicts a protein with a rel. mol. mass of 70,000 (mr 70K).
CC   The differences in translation products of the two clones do not
CC   result in detectable differences in transport properties.
XX
SQ   Sequence 2415 BP; 538 A; 700 C; 605 G; 572 T; 0 other;
```

```
  Query Match             32.8%;  Score 579.4;  DB 16;  Length 2415;
  Best Local Similarity   60.0%;  Pred. No. 1.5e-146;
  Matches  983;  Conservative    0;  Mismatches  651;  Indels    3;  Gaps    1;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145

Db        324 TGGTGGCTGAGATTCGCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 383

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205

Db        384 TGTCCGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 443

Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265

Db        444 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 503

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325

Db        504 TCCCGCTCTTTTACATGGAGCTCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCA 563

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385

Db        564 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 623

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445

Db        624 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 683

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505

Db        684 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 743

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565

Db        744 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 803

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625

Db        804 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 863

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685

Db        864 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 923

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745

Db        924 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 983

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805

Db        984 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1043

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865

Db       1044 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1103

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925

Db       1104 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1163

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985

Db       1164 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1223

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045

Db       1224 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1283

Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
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Db       1284 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1343

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
Db       1344 ATGCAGAGGCAATAGCCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1403

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db       1404 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1463

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db       1464 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1523

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
Db       1524 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1583

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
Db       1584 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1643

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
Db       1644 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1703

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
Db       1704 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1763

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
Db       1764 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1823

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
Db       1824 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1883

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
Db       1884 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGCATTATTA 1943

Qy       1703 CAATCCAACGTCCGGAA 1719
Db       1944 AAAGTATCACTCCTGAA 1960


SULT 4
Q41055
ID   AAQ41055 standard; cDNA; 2278 BP.
XX
AC   AAQ41055;
XX
DT   20-AUG-1993  (first entry)
XX
DE   Rat 5HT transporter cDNA.
XX
KW   Rat; 5HT; Serotonin transporter; psychological disorder;
KW   neurotransmitter; behavioural disorder; 5-hydroxytryptamine;
KW   antidepressants; depression.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             48..1868
FT                   /*tag=  a
XX
PN   WO9308261-A.
XX
PD   29-APR-1993.
XX
PF   21-OCT-1992;   92WO-US09095.
XX
PR   22-OCT-1991;   91US-0778231.
XX
PA   (UYDU-) UNIV DUKE.
PA   (UYEM-) UNIV EMORY.
XX
PI   Blakely RD,  Caron MG,  Fremeau RT;
XX
DR   WPI; 1993-152457/18.
DR   P-PSDB; AAR34662.
XX
PT   Serotonin transporter protein, its DNA and antibodies - for
PT   identifying serotonin transport inhibitors and probing serotonin
PT   transporter gene expression, e.g. to investigate genetic
PT   disorders
XX
PS   Claim 3; Page 37; 62pp; English.
XX
CC   This sequence is the rat 5HT transporter cDNA. It was isolated
CC   using a synthetic antisense oligonucleotide corresp. to the 5'end of
CC   a partial 5HT clone. This was used to screen a rat brainstem cDNA
CC   library. One positive plaque from a total screen of 1.2 * 10power6
CC   plaques was identified and the EcoR1 insert subcloned into
CC   pBluescript SKII.
XX
SQ   Sequence 2278 BP; 501 A; 657 C; 573 G; 547 T; 0 other;

  Query Match           32.7%;  Score 576.2;  DB 14;  Length 2278;
  Best Local Similarity   59.9%;  Pred. No. 1.1e-145;
  Matches  981;  Conservative    0;  Mismatches  653;  Indels    3;  Gaps    1;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
Db        187 TGGTGCCTGAGATTCGCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 246

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
Db        247 TGTCCGTCATCGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 306

Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
Db        307 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 366

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
Db        367 TCCCGCTCTTTTACATGGAGCTCGCACTGGGTCAGTACCACCGAAACGGGTGCATTTCCA 426

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
Db        427 TATCGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 486

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
Db        487 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 546

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
Db        547 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 606

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
Db        607 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 666

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
Db        667 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 726

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
Db        727 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 786

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
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Db        787 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 846

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
Db        847 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 906

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
Db        907 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 966

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
Db        967 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1026

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
Db       1027 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1086

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
Db       1087 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1146

Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
Db       1147 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1206

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
Db       1207 ATGCAGAGGCAATAGCCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1266

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db       1267 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1326

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db       1327 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1386

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
Db       1387 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1446

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
Db       1447 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1506

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
         1507 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1566

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
Db       1567 GCTTCAGCCCGGGATGGTTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1626

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
Db       1627 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1686

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
Db       1687 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1746

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
Db       1747 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGCATTATTA 1806

Qy       1703 CAATCCAACGTCCGGAA 1719
Db       1807 AAAGTATCACTCCTGAA 1823
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RESULT 5
AAQ41056

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ID   AAQ41056 standard; cDNA; 2415 BP.
XX
AC   AAQ41056;
XX
DT   20-AUG-1993  (first entry)
XX
DE   Rat 5HT transporter cDNA.
XX
KW   Rat; 5HT; Serotonin transporter; psychological disorder;
KW   neurotransmitter; behavioural disorder; 5-hydroxytryptamine;
KW   antidepressants; depression.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             115..2006
FT                   /*tag=  a
XX
PN   WO9308261-A.
XX
PD   29-APR-1993.
XX
PF   21-OCT-1992;   92WO-US09095.
XX
PR   22-OCT-1991;   91US-0778231.
XX
PA   (UYDU-) UNIV DUKE.
PA   (UYEM-) UNIV EMORY.
XX
PI   Blakely RD,  Caron MG,  Fremeau RT;
XX
DR   WPI; 1993-152457/18.
DR   P-PSDB; AAR34663.
XX
PT   Serotonin transporter protein, its DNA and antibodies - for
PT   identifying serotonin transport inhibitors and probing serotonin
PT   transporter gene expression, e.g. to investigate genetic
PT   disorders
XX
PS   Example 5; Page 43; 62pp; English.
XX
CC   This sequence is the rat 5HT transporter cDNA. It was isolated
CC   by further sequencing of the sequence isolated as in AAQ41055. This
CC   was found to have a gel compression error, whereby a G between 120-140
CC   was misread as GG. With this alteration it was found that the true
CC   start for translation was present in a reading frame upstream of the
CC   start site indicated in AAQ41055, thought to be a non coding sequence.
CC   The ORF encoding the transporter extends to 1890 bp predicting a protein
CC   of 630 amino acids with a RMM of 70kD. The differences in translation
CC   products between the two clones do not result in differences in
CC   transport properties.
XX
SQ   Sequence 2415 BP; 538 A; 707 C; 599 G; 571 T; 0 other;
```

Query Match 32.7%; Score 576; DB 14; Length 2415;
Best Local Similarity 60.2%; Pred. No. 1.2e-145;
Matches 973; Conservative 0; Mismatches 640; Indels 3; Gaps 1;

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Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db        345 GGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCCTGTCCGTCATTGGCTATGCCG 404

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db        405 TGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCTACCAGAATGGCGGAGGGGCCT 464

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db        465 TCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGATCCCGCTCTTTTACATGGAGC 524

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db        525 TCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCATATGGAGGAAGATCTGCCCGA 584
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Qy       347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db       585 TTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCTTTTACATCGCCTCCTACTACA 644

Qy       407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db       645 ACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCTCCCTCACGGACCGGCTGCCCT 704

Qy       467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db       705 GGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCACCAACTACTTCGCCCAGGACA 764

Qy       527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db       765 ACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGACGAGTTCTACTTGCGCCATGTCC 824

Qy       587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
Db       825 TGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCACCATCAGCTGGCAGCTGACTC 884

         647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
Db       885 TCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCATCTGGAAAGGCGTCAAAACAT 944

Qy       707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db       945 CTGCCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACATTGTCCTCTCTGTCCTGCTGG 1004

Qy       767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db      1005 TGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCGTCTTCTACTTGAAACCCAACT 1064

Qy       827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db      1065 GGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCGCCGCTCAGATCTTCTTCTCTC 1124

Qy       887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
Db      1125 TTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTCCTAGCTACAACAAGTTCAACAACAACT 1184

Qy       947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
Db      1185 GTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCATGACAAGCTTCGTCTCTGGCT 1244

Qy      1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db      1245 TCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGAGGAATGAAGATGTGTCAGAGG 1304

         1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db      1305 TGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGTATGCAGAGGCAATAGCCAACA 1364

Qy      1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db      1365 TGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCATGTTAATCACGCTGGGATTGG 1424

Qy      1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db      1425 ACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTGTGCTGGATGACTTCCCTCACA 1484

Qy      1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db      1485 TCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGGTCATCACGTGCGTCTTGGGAT 1544

Qy      1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
Db      1545 CCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGACTCTGCTGGAGGAGTATGCCA 1604

Qy      1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
Db      1605 CGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCGTCGCCGTGTCTTGGTTCTATG 1664

Qy      1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
Db      1665 GAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGGGCTTCAGCCCGGGATGGTTTT 1724

Qy      1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
Db      1725 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1784

Qy      1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
Db      1785 TGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACTATCCCCACTGGAGTATCGTCT 1844

Qy      1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
Db      1845 TGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCCCTACCTATATCATTTATCGGC 1904

Qy      1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAATCCAACGTCCGGAA 1719
Db      1905 TGATCAGCACTCCGGGGACACTTAAGGAGCGCATTATTAAAAGTATCACTCCTGAA 1960
```

RESULT 6
AAQ26646
ID AAQ26646 standard; DNA; 2756 BP.
XX
AC AAQ26646;
XX
DT 17-DEC-2001 (updated)
DT 19-JAN-1993 (first entry)
XX
DE Encodes 5HTT serotonin transporter.
XX
KW serotnin transporter protein; antidepressants; drug abuse;
KW amphetamines; cocaine; treating; diagnosing; neurological disorders;
KW ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   232..2190
FT   /*tag= a
FT   /product= serotonin transporter 5HTT
XX
PN USN7782298-N.
XX
PD 15-APR-1992.
XX
PF 24-OCT-1991; 91US-0782298.
XX
PR 24-OCT-1991; 91US-0782298.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Brownstein MJ, Hoffman BJ, Mezey E;
XX
DR WPI; 1992-259291/31.
DR P-PSDB; AAR25642.
XX
PT DNA clone encoding rat serotonin transport protein, 5 HTT -
PT useful in diagnosis and treatment of neurological disorders
XX
PS Example 1; Page 23; 47pp; English.
XX
CC This sequence encodes the 5HTT serotonin transporter. A cDNA
CC library was prepared in E. coli MC1061p3 from poly(A)+ RNA from
CC RBL 2H3 cells (cognate mast cells). Plasmid DNA was then prepared
CC and transfected into COS-7 cells, which were screened with 3H-5-HT
CC and a single positive pool identified microscopically and further
CC subdivided. These subdivisions were screened using degenerate
CC oligonucleotide probe AAQ26647, directed at a region highly conserved
CC in noradrenaline and GABA transporters. A single hybridising band
CC was present in each positive pool identified by bioassay through
CC three successive rounds of screening. A single positive clone was

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CC   isolated from a positive pool of 100 clones using this probe. 5HTT
CC   cDNA was subcloned into M13 bacteriphoage and sequenced completely
CC   on both strands.
CC   See also Q2644-50, AAR25642.
CC   (Note: Revised entry submitted to correct the patent number format of
CC   US Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.)
XX
SQ   Sequence 2756 BP; 624 A; 784 C; 687 G; 661 T; 0 other;

  Query Match           31.6%;  Score 557;  DB 13;  Length 2756;
  Best Local Similarity  59.6%;  Pred. No. 1.9e-140;
  Matches  976;  Conservative    0;  Mismatches  655;  Indels    6;  Gaps    2;

Qy         86 TGGTGTCGCTTACGCCGGCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGC 145
Db        440 TGGTGGCTGAGATTCCCCAAGGGGAGCGGGAGACCTGGGGCAAGAAGATGGATTTCCTCC 499

Qy        146 TGGCGGTGGTGGGATTCGCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTT 205
Db        500 TGTCCGTCATTGGCTATGCCGTGGACCTGGGCAACATCTGGCGGTTTCCTTACATATGCT 559

Qy        206 ACCAGAATGGAGGCGGTGCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGC 265
Db        560 ACCAGAATGGCGGAGGGGCCTTCCTCCTCCCTTATACCATCATGGCCATTTTCGGGGGGA 619

Qy        266 TGCCGCTGTTCTTCCTGGAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTC 325
Db        620 TCCCGCTCTTTTACATGGACCTCGCACTGGGCCAGTACCACCGAAACGGGTGCATTTCCA 679

Qy        326 TCTGGAAACGGATCTGCCCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACA 385
Db        680 TATGGAGGAAGATCTGCCCGATTTTCAAAGGCATTGGTTACGCCATCTGCATCATCGCCT 739

Qy        386 TCTACATGGGCATGTACTACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTT 445
Db        740 TTTACATCGCCTCCTACTACAACACCATCATAGCCTGGGCGCTCTACTACCTCATCTCCT 799

Qy        446 CTCTCGCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGC 505
Db        800 CCCTCACGGACCGGCTGCCCTGGACCAGCTGCACGAACTCCTGGAACACTGGCAACTGCA 859

Qy        506 CGCTGTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGG 565
Db        860 CCAACTACTTCGCCCAGGACAACATCACCTGGACGCTGCATTCCACGTCCCCCGCTGAGG 919

Qy        566 AGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGC 625
Db        920 AGTTCTACTTGCGCCATGTCCTGCAGATCCACCAGTCTAAGGGACTCCAGGACCTGGGCA 979

Qy        626 CGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCT 685
Db        980 CCATCAGCTGGCAGCTGACTCTCTGCATCGTGCTCATCTTCACCGTAATCTACTTTAGCA 1039

Qy        686 TGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACG 745
Db       1040 TCTGGAAAGGCGTCAAAACATCTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCATACA 1099

Qy        746 TGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATAC 805
Db       1100 TTGTCCTCTCTGTCCTGCTGGTGAGGGGGGCCACCCTTCCTGGAGCCTGGAGAGGGGTCG 1159

Qy        806 GCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGG 865
Db       1160 TCTTCTACTTGAAACCCAACTGGCAGAAACTCTTGGAGACAGGGGTGTGGGTAGATGCCG 1219

Qy        866 CATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCT 925
Db       1220 CCGCTCAGATCTTCTTCTCTCTTGGCCCGGGCTTTGGGGTTCTCCTGGCTTTTGCTAGCT 1279

Qy        926 ACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCT 985
Db       1280 ACAACAAGTTCAACAACAACTGTTACCAAGATGCCCTGGTGACCAGTGTGGTGAACTGCA 1339

Qy        986 TGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTC 1045
Db       1340 TGACAAGCTTCGTCTCTGGCTTCGTCATCTTCACGGTGCTTGGCTACATGGCGGAGATGA 1399

Qy       1046 AGAACAAGAGCATCGAGGAGGTTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGT 1102
Db       1400 GGAATGAAGATGTGTCAGAGGTGGCCAAAGACGCAGGCCCCAGCCTCCTCTTCATCACGT 1459

Qy       1103 ACCCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCA 1162
Db       1460 ATGCAGAGGCAATAGGCAACATGCCAGCATCCACGTTCTTTGCCATCATCTTCTTCCTCA 1519

Qy       1163 TGCTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTC 1222
Db       1520 TGTTAATCACGCTGGGATTGGACAGCACGTTCGCAGGCCTGGAAGGTGTGATCACAGCTG 1579

Qy       1223 TTTGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGC 1282
Db       1580 TGCTGGATGAGTTCCCTCACATCTGGGCCAAGCGCAGGGAATGGTTCGTGCTCATCGTGG 1639

Qy       1283 TTCTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAG 1342
Db       1640 TCATCACGTGCGTCTTGGGATCCCTGCTCACACTGACGTCAGGAGGGGCATACGTGGTGA 1699

Qy       1343 ACCTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTG 1402
Db       1700 CTCTGCTGGAGGAGTATGCCACGGGGCCAGCAGTGCTCACCGTGGCCCTCATCGAGGCCG 1759

Qy       1403 CCGGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGG 1462
Db       1760 TCGCCGTGTCTTGGTTCTATGGAATCACTCAGTTCTGCAGCGATGTGAAGGAGATGCTGG 1819

Qy       1463 GGCACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGC 1522
Db       1820 GCTTCAGC---GGGATGGTTTGGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCC 1876

Qy       1523 TGGTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCT 1582
Db       1877 TGTTCATCATTTGCAGTTTTCTGATGAGCCCACCCCAGCTACGGCTTTTCCAATACAACT 1936

Qy       1583 ATCCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTC 1642
Db       1937 ATCCCCACTGGAGTATCGTCTTGGGCTACTGCATAGGGATGTCGTCCGTCATCTGCATCC 1996

Qy       1643 CTCTTTACATTATCTACAAACTGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGA 1702
Db       1997 CTACCTATATCATTTATCGGCTGATCAGCACTCCGGGGACACTTAAGGAGCGGATTATTA 2056

Qy       1703 CAATCCAACGTCCGGAA 1719
Db       2057 AAAGTATCACTCCTGAA 2073


RESULT 7
AAF73818
ID   AAF73818 standard; DNA; 1890 BP.
XX
AC   AAF73818;
XX
DT   30-APR-2001  (first entry)
XX
DE   Partial human SLC6A4 DNA #11.
XX
KW   Solute carrier family 6 neurotransmitter transporter; seotonin 4;
KW   SLC6A4; genotyping; allele specific oligonucleotide; ds.
XX
OS   Homo sapiens.
XX
PN   WO200109161-A1.
XX
PD   08-FEB-2001.
```

XX
PF 31-JUL-2000; 2000WO-US20638.
XX
PR 29-JUL-1999; 99US-0146290.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Duda A, Nandabalan K, Sanchis A, Stephens JC;
XX
DR WPI; 2001-123317/13.
XX
PT New isolated polynucleotide comprising a polymorphic variant for the
PT solute carrier family 6 neurotransmitter transporter, serotonin member
PT 4 gene for identifying drugs for treating disorders related to
PT expression of the protein -
XX
PS Claim 7; Fig 11; 152pp; English.
XX
CC The present invention relates to a polymorphic variant of a reference
CC sequence for the solute carrier family 6 neurotransmitter
CC transporter, serotonin member 4 (SLC6A4) gene or a fragment of it
CC or a sequence complementary to the first sequence.
CC The invention is used in producing a recombinant organism
CC that can be used to express SLC6A4 for protein structure analysis and
CC binding studies. A composition comprising a genotyping oligonucleotide
CC is used to detect a polymorphism in the SLC6A4 gene.
XX
SQ Sequence 1890 BP; 406 A; 510 C; 489 G; 485 T; 0 other;

Query Match 31.4%; Score 554; DB 22; Length 1890;
Best Local Similarity 59.6%; Pred. No. 1e-139;
Matches 954; Conservative 0; Mismatches 645; Indels 3; Gaps 1;

```
Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
              || | || ||||||||||  |||||||  || |||||  ||  | ||| | || |  || |
Db        230 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 289

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
              ||||  || || || || ||||| |||||||||||  ||||||||||||||||||  || || |
Db        290 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 349

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
              ||||  |||| |||  | | |||    | ||||| ||  | ||||| || | | |||| |
Db        350 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 409

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
              | || ||||| ||||||||||    || ||| |  |  | ||||     ||||||||
Db        410 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 469

          347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
                | |||||| | || ||||||||||||||| || | | | ||||| |     |||||||
Db        470 TTTTCAAAGGTATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 529

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
              ||||  ||||| |  |||||| | || ||||| ||| | ||  || ||          |
Db        530 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 589

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
                |   || |  | || |   |||    | |||    |    | |    | |     |
Db        590 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 649

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
                      |  |   | ||  |  | || ||  | || || | |   ||  | ||
Db        650 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 709

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
              || ||   |||  |||||| || ||  | ||| |||||   ||||    | ||||||  |
Db        710 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 769

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
              | ||  |  |   | ||||      | ||||||||  | | ||||||||| |||| ||
Db        770 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 829

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
              ||||||||||||||||||||||||||       ||| ||  |  | ||     | |||||||
Db        830 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 889

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
              ||| || | ||| || || |||||   |  |||  | | || |||| | |  ||  | |
Db        890 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 949

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
              |||| ||| | |   |  |   ||| |||||  || || ||  | |||||  |||||||| |
Db        950 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1009

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
              | ||||| || || ||   ||| |||||   |  | ||||||||||||||||||||||||
Db        1010 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1069

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
              |||||   || || ||  | ||         | |||||| |||| |||||| || | || |
Db        1070 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1129

Qy        1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
               | ||||| ||| | ||  | || ||||||||  |  |   |||  |      |    ||||
Db        1130 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1189

Qy        1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
               | | |     || ||| ||  | ||  | ||||||  |||  | || || || |||| ||
Db        1190 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1249

Qy        1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
               || | |  |||   ||||  |||||||||||||| || ||| | || || |||||  | |
Db        1250 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1309

Qy        1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
               |||| || |||| ||| | ||||  || | |||||||  |    || || |  || |  |
Db        1310 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1369

Qy        1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
               | |  | ||  | || ||   || |||   |   || |  |   |  |  ||   || |
Db        1370 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1429

Qy        1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
               | |||  ||||   || |  || || |  ||| | ||  | || ||  | | |||||  |
Db        1430 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1489

Qy        1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
               | ||    ||  | ||    || |   |    || || | ||  ||||  ||| | ||||
Db        1490 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1549

Qy        1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
               || ||   | |||||    || |||| |   |||||  ||   ||  ||| || ||||||||
Db        1550 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1609

Qy        1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
               |||||| ||| |||     |||||| ||  | ||  | ||| |  |  |       |
Db        1610 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1669

Qy        1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
               | ||    |     | | |        |||| |  ||||| |  |||  |||||  |
Db        1670 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1729

Qy        1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
               | || |     ||       | |  |  ||  ||||| ||    || ||    ||
Db        1730 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1789

Qy        1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
               || |||||||||| || |  |  |  | || || |  | ||
Db        1790 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1831
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RESULT 8
AAQ41057
ID AAQ41057 standard; cDNA; 2508 BP.
XX

```
AC   AAQ41057;
XX
DT   20-AUG-1993  (first entry)
XX
DE   Human 5HT transporter cDNA.
XX
KW   Rat; 5HT; Serotonin transporter; psychological disorder;
KW   neurotransmitter; behavioural disorder; 5-hydroxytryptamine;
KW   antidepressants; depression.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73..1962
FT                   /*tag=  a
XX
PN   WO9308261-A.
XX
PD   29-APR-1993.
XX
PF   21-OCT-1992;   92WO-US09095.
XX
PR   22-OCT-1991;   91US-0778231.
XX
PA   (UYDU-) UNIV DUKE.
PA   (UYEM-) UNIV EMORY.
XX
PI   Blakely RD,  Caron MG,  Fremeau RT;
XX
DR   WPI; 1993-152457/18.
DR   P-PSDB; AAR34664.
XX
PT   Serotonin transporter protein, its DNA and antibodies - for
PT   identifying serotonin transport inhibitors and probing serotonin
PT   transporter gene expression, e.g. to investigate genetic
PT   disorders
XX
PS   Claim 2; Page 49; 62pp; English.
XX
CC   This sequence is the human 5HT transporter cDNA. Poly A+ RNA
CC   purified from a placental trophoblastic cell line was converted to
CC   single stranded cDNA and subjected to PCR using AAQ41058,9 designed to
CC   encode highly conserved sequences of NE and GABA transporters and that
CC   had been previously employed for the identification of the rat brain 5HT
CC   transporter. Following direct cloning of PCR fragments sequencing was
CC   performed on plasmid DNA to identify partial  human 5HT transporter
CC   candidates. A synthetic 21mer oligonucleotide AAQ41060 derived from the
     5'end of the JAR cDNA was 3'end labeled with GAMMA32P atp and used to
     screen a human placental cDNA library in lambdaZAPII by Magnagraph (MSI)
     filter hybridisation. 3 hybridising clones were identified in a screen
CC   of 1.6*10power6 plaques, and following rescreening were obtained as
CC   individual plasmids by in vivo excision. Restriction and sequencing
CC   analysis revealed two of these clones to be homologous to rSERT and to
CC   be identical with each other except for the presence of distinct
CC   deletions in each DNA. A recombination PCR approach was then used to
CC   ligate in-frame the two pieces possessed uniquely by the two cDNAs which
CC   was transferred back into the original clone at convenient restriction
CC   sites.
XX
SQ   Sequence 2508 BP; 572 A; 652 C; 631 G; 653 T; 0 other;
```

Query Match 31.3%; Score 552.4; DB 14; Length 2508;
Best Local Similarity 59.5%; Pred. No. 3.2e-139;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

```
Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db        662 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db       1382 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
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Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423

Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483

Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543

Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705

Db       1862 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1903
```

RESULT 9
AAQ94018
ID AAQ94018 standard; cDNA; 2508 BP.
XX
AC AAQ94018;
XX
DT 02-DEC-1995 (first entry)
XX
DE Human 5HT transporter (hSERT).
XX
KW Serotonin transporter; 5-hydroxytryptamine; 5HT; noradrenaline; NA;
KW SERT; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 73..1962
FT /*tag= a
XX
PN US5418162-A.
XX
PD 23-MAY-1995.
XX
PF 22-OCT-1991; 91US-0778231.
XX
PR 14-OCT-1992; 92US-0959943.
PR 22-OCT-1991; 91US-0778231.
XX
PA (UYDU-) UNIV DUKE.
PA (UYEM-) UNIV EMORY.
XX
PI Blakely RD, Caron MG, Fremeau RT;
XX
DR WPI; 1995-199742/26.
DR P-PSDB; AAR76074.
XX
PT DNA encoding rat serotonin transporter - useful in the rational design of
PT drugs and for screening for RFLP associated with certain disorders
XX
PS Claim 12; column 37-42; 27pp; English.
XX
CC An oligo probe capable of hybridising to a DNA consisting of a
CC portion of AAQ94018 is claimed. Poly (A+) RNA purified from a
CC placental trophoblastic cell line is used to prepare a human
CC placental cDNA library. A synthetic oligo based on partial
CC human 5HT transporter candidates was used to screen the
CC library. Three hybridising clones were identified. Two of these
CC clones were found to be homologous to rSERT and to be
CC identical with each other except for the presence of distinct
CC deletions in each cDNA. A PCR approach was used to ligate in-frame
CC the two pieces possessed uniquely by the two cDNAs.
XX
SQ Sequence 2508 BP; 572 A; 652 C; 631 G; 653 T; 0 other;

Query Match 31.3%; Score 552.4; DB 16; Length 2508;
Best Local Similarity 59.5%; Pred. No. 3.2e-139;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

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Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166

Db        302 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 361

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226

Db        362 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 421

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286

Db        422 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 481

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346

Db        482 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 541

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406

Db        542 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 601

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466

Db        602 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 661

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526

Db        662 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 721

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586

Db        722 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 781

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646

Db        782 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 841

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706

Db        842 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 901

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766

Db        902 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 961

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826

Db        962 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1021

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886

Db       1022 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1081

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946

Db       1082 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1141

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006

Db       1142 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1201
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Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
Db       1202 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1261

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
Db       1262 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1321

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
Db       1322 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1381

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
Db       1382 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1441

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303
Db       1442 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1501

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
Db       1502 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1561

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
Db       1562 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1621

Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
Db       1622 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1681

Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
Db       1682 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1741

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603
Db       1742 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 1801

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663
Db       1802 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 1861

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
Db       1862 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 1903
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RESULT 10
AAX57846
ID AAX57846 standard; DNA; 2889 BP.
XX
AC AAX57846;
XX
DT 15-JUL-1999 (first entry)
XX
DE Human serotonin transporter coding sequence.
XX
KW YAC; yeast artificial chromosome; serotonin transporter; SERT;
KW reporter gene; transgenic mammal; therapy; circadian function; human;
KW sleep disorder; eating disorder; premenstrual syndrome; birth defect;
KW autoimmune disorder; sexual dysfunction; ss.
XX
OS Homo sapiens.
XX
PN GB2331752-A.
XX
PD 02-JUN-1999.
XX
PF 27-NOV-1998; 98GB-0026126.
XX
PR 05-NOV-1998; 98GB-0024275.
PR 28-NOV-1997; 97GB-0025311.
PR 28-NOV-1997; 97GB-0025313.
PR 20-MAR-1998; 98GB-0006072.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Harmar AJ, Schedl A, Shen S;
XX
DR WPI; 1999-290603/25.
XX
PT New reporter gene labeled YAC vectors and transgenic mammals used
PT for screening potential active agents
XX
PS Disclosure; Page 70-71; 98pp; English.
XX
CC This sequence encodes the human serotonin transporter (SERT).
CC The invention relates to yeast artificial chromosome (YAC) vectors
CC containing a reporter gene and transgenic mammals produced using them may
CC be used to screen for an agent affecting nucleotide expression and gives
CC easier monitoring of in vivo expression. The vector is used in the
CC production of transgenic mammals for testing potential pharmaceutical or
CC veterinary agents. pYAM4 is used to amplify YAC. The assay may be used to
CC screen for agents useful in treatment of disturbance of circadian
CC function, sleep disorders, eating disorders, premenstrual syndrome,
CC autoimmune disorders, birth defects in women and/or sexual dysfunction.
CC The agents thus detected may be used for treatment of disorders related
CC to the expression pattern of a nucleotide such as those above. The
CC vectors have more concentrated YAC DNA, which allows better and more
CC reliable gene transfer. The presence of a reporter gene allows easy
CC monitoring of in vivo expression and the vectors allow for gene
CC overexpression (3-5 fold) and easy site determination. The pYAM4
CC amplification vector does not contain the thymidine kinase gene, which
CC causes male infertility in transgenic mice.
XX
SQ Sequence 2889 BP; 672 A; 753 C; 722 G; 742 T; 0 other;

Query Match 31.3%; Score 552.4; DB 20; Length 2889;
Best Local Similarity 59.5%; Pred. No. 3.4e-139;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

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Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
Db        535 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 594

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
Db        595 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 654

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
Db        655 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 714

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
Db        715 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 774

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
Db        775 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 834

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
Db        835 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 894

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
Db        895 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 954

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
Db        955 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 1014

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
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Db       1015 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 1074

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706

Db       1075 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 1134

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766

Db       1135 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 1194

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826

Db       1195 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1254

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886

Db       1255 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1314

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946

Db       1315 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1374

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006

Db       1375 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1434

Qy       1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066

Db       1435 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1494

Qy       1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123

Db       1495 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1554

Qy       1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183

Db       1555 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1614

Qy       1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243

Db       1615 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1674

Qy       1244 TGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTTCTGTTCATCTATATTTGCG 1303

Db       1675 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1734

Qy       1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363

b        1735 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1794

Qy       1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423

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Qy       1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483

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Qy       1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543

Db       1915 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1974

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1975 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 2034

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       2035 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 2094

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705
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Db       2095 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 2136


RESULT 11
AAC85219
ID   AAC85219 standard; DNA; 2889 BP.
XX
AC   AAC85219;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Human serotonin transporter gene.
XX
KW   Internal ribosomal entry site; IRES; yeast artificial chromosome;
KW   YAC; vector; centromere; telomere; origin of replication;
KW   transgenic; circadian function; sleep disorder; eating disorder;
KW   premenstrual syndrome; autoimmune disease; birth defect;
KW   sexual dysfunction; serotonin transporter; VIP2 receptor; SERT;
KW   VIPR2; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   exon            86..182
FT                   /*tag=  b
FT                   /label= Exon 1B
FT                   /note= "Some splice variants do not include this
FT                   exon"
FT   exon            183..648
FT                   /*tag=  c
FT                   /label= Exon 2
FT   exon            649..783
FT                   /*tag=  d
FT                   /label= Exon 3
FT   exon            784..1003
FT                   /*tag=  e
FT                   /label= Exon 4
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FT   exon            1143..1277
FT                   /*tag=  g
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FT                   /*tag=  h
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FT   exon            1382..1509
FT                   /*tag=  i
FT                   /label= Exon 8
FT   exon            1510..1622
FT                   /*tag=  j
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FT   exon            1623..1754
FT                   /*tag=  k
FT                   /label= Exon 10
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FT                   /*tag=  l
FT                   /label= Exon 11
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FT                   /label= Exon 12
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FT                   /*tag=  n
FT                   /label= Exon 13
FT   exon            2124..2889
FT                   /*tag=  o
FT                   /label= Exon 14
FT   CDS             180..2198
FT                   /*tag=  p
FT                   /product= SERT
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PN GB2350613-A.
XX
PD 06-DEC-2000.
XX
PF 17-AUG-2000; 2000GB-0020335.
XX
PR 28-NOV-1997; 97GB-0025311.
PR 28-NOV-1997; 97GB-0025313.
PR 20-MAR-1998; 98GB-0006072.
PR 05-NOV-1998; 98GB-0024275.
PR 27-NOV-1998; 98GB-0026126.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Shen S, Schedl A, Harmar AJ;
XX
DR WPI; 2001-034098/05.
XX
PT Transgenic organism for identifying potential therapeutic agents able
PT to modulate gene expression, comprises a yeast artificial chromosome
PT vector
XX
PS Disclosure; Page 67-68; 93pp; English.
XX
CC The sequences given in AAC85219-220 represent nucleotide sequences of
CC interest (NOI) which were used in the construction of a yeast
CC artificial chromosome (YAC) vector (V1). (V1) comprises a centromere,
CC two telomeres, at least one origin of replication, an internal
CC ribosomal entry site (IRES), and a selection gene that is specifically
CC removable from the vector. YAC prepared from the new vectors are
CC used to produce transgenic organisms for use in screening for
CC agents that can affect the expression pattern of an NOI or the
CC activity of its expression product (EP). The identified agents are
CC potentially useful as pharmaceutical and veterinary agents for
CC treating disorders of circadian function; sleep or eating disorders;
CC premenstrual syndrome; autoimmune diseases; birth defects in women
CC and/or sexual dysfunction, and also as lead compounds for developing
CC agents with other activities. YAC can also be used for expression,
CC regulation and/or functional studies on NOI, in combination with other
CC NOI, compounds or compositions. The new vectors provide high YAC copy
CC numbers and allow easy monitoring (in vivo) of the expression pattern
CC of NOI; (over)expression of NOI and a reporter gene; and determination
CC of the sites where NOI is expressed. Incorporation of IRES allows
CC expression of at least two nucleic acid sequences (e.g. NOI plus a
CC reporter of more than one NOI).
XX
SQ Sequence 2889 BP; 672 A; 753 C; 722 G; 742 T; 0 other;

Query Match 31.3%; Score 552.4; DB 22; Length 2889;
Best Local Similarity 59.5%; Pred. No. 3.4e-139;
Matches 953; Conservative 0; Mismatches 646; Indels 3; Gaps 1;

```
Qy        107 GGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTCGCAG 166
              || | || ||||||||||  |||||||  || |||||  ||  | ||| | || |  || |
Db        535 GGGAACGGGAGACCTGGGGCAAGAAGGTGGATTTCCTTCTCTCAGTGATTGGCTATGCTG 594

Qy        167 TGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGTGCGT 226
              ||||  || ||  ||  || |||||  |||||||||||  ||||||||||||||||||  || || |
Db        595 TGGACCTGGGCAATGTCTGGCGCTTCCCCTACATATGTTACCAGAATGGAGGGGGGGCAT 654

Qy        227 TCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTGGAAC 286
              ||||  |||| |||  | | |||    | |||||  ||  | |||||  || | | |||| |
Db        655 TCCTCCTCCCCTACACCATCATGGCCATTTTTGGGGGAATCCCGCTCTTTTACATGGAGC 714

Qy        287 TGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGCCCCG 346
              | || |||||  ||||||||||    || ||| |  |  | ||||     ||||||||
Db        715 TCGCACTGGGACAGTACCACCGAAATGGATGCATTTCAATATGGAGGAAAATCTGCCCGA 774

Qy        347 CGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTACTACA 406
                | |||||  | || ||||||||||||||  || | | | |||||  |     |||||||
Db        775 TTTTCAAAGGGATTGGTTATGCCATCTGCATCATTGCCTTTTACATTGCTTCCTACTACA 834

Qy        407 ACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTCTCTCGCGTCTATAAACTCTG 466
              |||| ||||| |  |||||| | || ||||| ||| | ||  ||  ||           |
Db        835 ACACCATCATGGCCTGGGCGCTATACTACCTCATCTCCTCCTTCACGGACCAGCTGCCCT 894

Qy        467 TGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCTGTGCACGCCGGTCACCT 526
              |      || | | || |  |||    | |||    |   | |   | |   |
Db        895 GGACCAGCTGCAAGAACTCCTGGAACACTGGCAACTGCACCAATTACTTCTCCGAGGACA 954

Qy        527 CACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAGGAGTTCTTCGAACGTAATGTAT 586
                  |  | || |  | || ||  | || ||  | |   ||  | ||
Db        955 ACATCACCTGGACCCTCCATTCCACGTCCCCTGCTGAAGAATTTTACACGCGCCACGTCC 1014

Qy        587 TGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGGCCGATCAAGCCGTCGCTGGCTC 646
              || ||   |||  |||||| || ||  | ||| |||||   ||||    |  |||||| |
Db        1015 TGCAGATCCACCGGTCTAAGGGGCTCCAGGACCTGGGGGGCATCAGCTGGCAGCTGGCCC 1074

Qy        647 TGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCCTTGTGGAAAGGAGTCAGGAGTG 706
              | ||  |  |  | ||||      |  |||||||  | | ||||||| |||| ||
Db        1075 TCTGCATCATGCTGATCTTCACTGTTATCTACTTCAGCATCTGGAAAGGCGTCAAGACCT 1134

Qy        707 CTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTACGTGGTGCTGCTGATTCTGCTGG 766
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Db        1135 CTGGCAAGGTGGTGTGGGTGACAGCCACCTTCCCTTATATCATCCTTTCTGTCCTGCTGG 1194

Qy        767 CGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATACGCTACTACCTTACCCCAGAGT 826
              ||| || | ||| || || |||||    |  |||  | | ||| | | ||  | |
Db        1195 TGAGGGGTGCCACCCTCCCTGGAGCCTGGAGGGGTGTTCTCTTCTACTTGAAACCCAATT 1254

Qy        827 GGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCGGCATCCCAGATTTTCTTCTCGC 886
              |||| ||| | |   | |   ||| ||||| || || ||  | ||||| ||||||||  |
Db        1255 GGCAGAAACTCCTGGAGACAGGGGTGTGGATAGATGCAGCCGCTCAGATCTTCTTCTCTC 1314

Qy        887 TCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGCTACAACAAGTTCAACAACAACT 946
              | ||||| || || ||   ||| |||||  |  | ||||||||||||||||||||||||
Db        1315 TTGGTCCGGGCTTTGGGGTCCTGCTGGCTTTTGCTAGCTACAACAAGTTCAACAACAACT 1374

Qy        947 GCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGCTTGACCAGCTTCCTTGCTGGTT 1006
              |||||   || || ||  | ||        | ||||||  |||| ||||||  || | || |
Db        1375 GCTACCAAGATGCCCTGGTGACCAGCGTGGTGAACTGCATGACGAGCTTCGTTTCGGGAT 1434

Qy        1007 TCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTTCAGAACAAGAGCATCGAGGAGG 1066
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Db        1435 TTGTCATCTTCACAGTGCTCGGTTACATGGCTGAGATGAGGAATGAAGATGTGTCTGAGG 1494

Qy        1067 TTGGC---CTCGAAGGCCCTGGACTGGTGTTCATCGTGTACCCCGAGGCCATCGCCACCA 1123
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Db        1495 TGGCCAAAGACGCAGGTCCCAGCCTCCTCTTCATCACGTATGCAGAAGCGATAGCCAACA 1554

Qy        1124 TGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATGCTTATTACCCTGGGACTTG 1183
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Db        1555 TGCCAGCGTCCACTTTCTTTGCCATCATCTTCTTTCTGATGTTAATCACGCTGGGCTTGG 1614

Qy        1184 ACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTTTGCGACGAATATCCTCGAG 1243
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Db        1615 ACAGCACGTTTGCAGGCTTGGAGGGGGTGATCACGGCTGTGCTGGATGAGTTCCCACACG 1674

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Db        1675 TCTGGGCCAAGCGCCGGGAGCGGTTCGTGCTCGCCGTGGTCATCACCTGCTTCTTTGGAT 1734

Qy        1304 CTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGACCTACTCAATGTGTATGGCC 1363
               | |||  ||||   || |  || || |  ||| | ||  | || ||  | | |||||  |
Db        1735 CCCTGGTCACCCTGACTTTTGGAGGGGCCTACGTGGTGAAGCTGCTGGAGGAGTATGCCA 1794

Qy        1364 CTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCCGGCGTGTGCTGGGTGTATG 1423
               | ||   ||  | ||   || |   |   || || | ||  |||| |||  | ||||
Db        1795 CGGGGCCCGCAGTGCTCACTGTCGCGCTGATCGAAGCAGTCGCTGTGTCTTGGTTCTATG 1854

Qy        1424 GCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGGCACACCCCTGGATGGTTCT 1483
               || ||   | ||||     || |||| |   ||||| ||   || ||| || |||||||
Db        1855 GCATCACTCAGTTCTGCAGGGACGTGAAGGAAATGCTCGGCTTCAGCCCGGGGTGGTTCT 1914

Qy        1484 GGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTGGTGCTGTTCGTGTTCTCCG 1543
```

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Db       1915 GGAGGATCTGCTGGGTGGCCATCAGCCCTCTGTTTCTCCTGTTCATCATTTGCAGTTTTC 1974

Qy       1544 TTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTATCCCTCATGGTCTATCACCG 1603

Db       1975 TGATGAGCCCGCCACAACTACGACTTTTCCAATATAATTATCCTTACTGGAGTATCATCT 2034

Qy       1604 TAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCTCTTTACATTATCTACAAAC 1663

Db       2035 TGGGTTACTGCATAGGAACCTCATCTTTCATTTGCATCCCCACATATATAGCTTATCGGT 2094

Qy       1664 TGCTCATCACTCCTGGCAATTGCATCAACCGCATCAAGACAA 1705

Db       2095 TGATCATCACTCCAGGGACATTTAAAGAGCGTATTATTAAAA 2136


RESULT 12
AAH28082
ID   AAH28082 standard; DNA; 1854 BP.
XX
AC   AAH28082;
XX
DT   05-SEP-2001 (first entry)
XX
DE   Nucleotide sequence of a human norepinephrine transporter.
XX
KW   Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW   mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW   amphetamine abuse; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1854
FT                   /*tag= a
FT                   /product= "norepinephrine transporter"
XX
PN   WO200148246-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35491.
XX
PR   29-DEC-1999;   99US-0173682.
PR   11-JAN-2000; 2000US-0175456.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Robertson D,  Blakely RD;
XX
DR   WPI; 2001-425681/45.
DR   P-PSDB; AAB84532.
XX
PT   Screening for susceptibility to sub-optimal norepinephrine transport,
PT   particularly orthostatic intolerance in a subject by detecting a
PT   polymorphism of norepinephrine transporter gene -
XX
PS   Claim 75; Page 98-101; 133pp; English.
XX
CC   The present sequence encodes a human norepinephrine transporter. The
CC   specification a method for screening for susceptibility to sub-optimal
CC   norepinephrine (NE) transport in a subject. The method comprises
CC   obtaining a biological sample from the subject and detecting a
CC   polymorphism of a norepinephrine transporter gene in the sample from
CC   the subject, the presence of the polymorphism indicating the
CC   susceptibility of the subject to sub-optimal norepinephrine transport.
CC   The method is useful for screening for susceptibility of a subject to
CC   orthostatic intolerance. Norepinephrine transporter genes are useful
CC   for gene therapy for modulating norepinephrine transport in a target
CC   cell and treating susceptibility to impaired norepinephrine transporter
CC   function, orthostatic intolerance or other relevant diseases in humans
CC   and animals such as mental illness, hypertension, heart disease, psycho
CC   stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ   Sequence 1854 BP; 356 A; 554 C; 494 G; 450 T; 0 other;

  Query Match           29.6%;  Score 522.4;  DB 22;  Length 1854;
  Best Local Similarity   59.9%;  Pred. No. 3.7e-131;
  Matches  956;  Conservative    0;  Mismatches  616;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162

Db        157 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 216

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222

Db        217 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 276

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282

Db        277 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 336

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342

Db        337 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 393

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402

Db        394 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 453

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC----------TCTC 450

Db        454 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 513

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509

Db        514 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 573

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564

Db        574 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 633

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624

Db        634 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 693

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684

Db        694 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 753

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744

Db        754 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 813

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804

Db        814 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 873

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864

Db        874 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 933

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924

Db        934 GCAACTCAGATATTTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 993

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984

Db        994 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1053

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044

Db       1054 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1113

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
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Db       1114 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1173

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
             || ||||||||  | ||| || | || ||    ||||||||  |  | || ||| |||||
Db       1174 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1233

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
             ||  |  | ||||| ||||||||  |  | |||||  | |||||  |||| |||||  ||
Db       1234 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1293

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
                || || |     |  ||  |     |||| ||  || | ||      ||   |
Db       1294 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1350

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
               |   ||  |   ||  ||| |||  |  ||  ||  | |||||  | ||| || |   |
Db       1351 TTCAGCACTTTCCTTCTCGCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1410

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
             || ||  |    | ||   | ||     | || || || |  ||  |    || ||   |
Db       1411 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1470

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
             || || | |||| | ||||| || ||| |||||    | ||  |   |   ||| |||||
Db       1471 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1530

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
               ||  || ||    | ||||||    || |||   | | |||||| |  ||| | |||
Db       1531 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1590

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
               |  || | ||| ||  | |  |     | ||    |   |  ||  || |||| ||
Db       1591 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACTACATCTTC 1650

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
             ||  | ||| | | |   || || |||  ||  ||    || || |        | ||
Db       1651 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1710

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680
               | ||| | ||||| ||  | |||| ||| |  |||
Db       1711 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 1746


RESULT 13
AAH28086
ID   AAH28086 standard; DNA; 1854 BP.
XX
     AAH28086;

     05-SEP-2001  (first entry)
XX
DE   Nucleotide sequence of a human norepinephrine transporter.
XX
KW   Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW   mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW   amphetamine abuse; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1854
FT                   /*tag= a
FT                   /product= "norepinephrine transporter"
XX
PN   WO200148246-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US35491.
XX
PR   29-DEC-1999;  99US-0173682.
PR   11-JAN-2000; 2000US-0175456.
XX
PA   (UYVA-) UNIV VANDERBILT.
XX
PI   Robertson D,  Blakely RD;
XX
DR   WPI; 2001-425681/45.
DR   P-PSDB; AAB84534.
XX
PT   Screening for susceptibility to sub-optimal norepinephrine transport,
PT   particularly orthostatic intolerance in a subject by detecting a
PT   polymorphism of norepinephrine transporter gene  -
XX
PS   Claim 75; Page 112-115; 133pp; English.
XX
CC   The present sequence encodes a human norepinephrine transporter. The
CC   specification a method for screening for susceptibility to sub-optimal
CC   norepinephrine (NE) transport in a subject. The method comprises
CC   obtaining a biological sample from the subject and detecting a
CC   polymorphism of a norepinephrine transporter gene in the sample from
CC   the subject, the presence of the polymorphism indicating the
CC   susceptibility of the subject to sub-optimal norepinephrine transport.
CC   The method is useful for screening for susceptibility of a subject to
CC   orthostatic intolerance. Norepinephrine transporter genes are useful
CC   for gene therapy for modulating norepinephrine transport in a target
CC   cell and treating susceptibility to impaired norepinephrine transporter
CC   function, orthostatic intolerance or other relevant diseases in humans
CC   and animals such as mental illness, hypertension, heart disease, psycho
CC   stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ   Sequence 1854 BP; 357 A; 553 C; 494 G; 450 T; 0 other;

  Query Match             29.6%;  Score 522.4;  DB 22;  Length 1854;
  Best Local Similarity   59.9%;  Pred. No. 3.7e-131;
  Matches  956;  Conservative    0;  Mismatches  616;  Indels   24;  Gaps    4;

Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
              |||| ||  || ||||||||||  ||||||   || |||||||||  | || || || |||
Db        157 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 216

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
              |||||||| || |  |||||||||| |||||||| |||| ||| |||| || ||||||
Db        217 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 276

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
              || ||| ||||||||||     |  | ||  |  | |  ||| |||| ||||||| | ||
Db        277 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 336

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
              || ||||| ||||| |||||| ||||    ||      |||  | ||||||   ||||||
Db        337 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 393

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
              ||     | ||||| || |||||||  ||  | ||||||  | | ||| | ||| | |||
Db        394 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 453

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC------------TCTC 450
              ||||||   |||||||  ||| |  | || |||||  || | ||           ||
Db        454 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 513

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509
               | |  |   ||| ||  |   | |||| ||||  | ||           || ||  ||
Db        514 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 573

Qy        510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564
                    | |  ||  | || |    |  ||           ||   |  || |||||
Db        574 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 633

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624
              ||||| |  || |||  |||  || | |  ||| ||   | |||  |  |||||||  ||
Db        634 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 693

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684
              | |  | ||  |  |||    || ||| || | |  ||| |  || || | || ||   |
Db        694 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 753
```

```
Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744
Db        754 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 813

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804
Db        814 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 873

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864
Db        874 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 933

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924
Db        934 GCAACTCAGATATTTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 993

Qy        925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984
Db        994 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1053

          985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044
Db       1054 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1113

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
Db       1114 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1173

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
Db       1174 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1233

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
Db       1234 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1293

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
Db       1294 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1350

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
Db       1351 TTCAGCACTTTCCTTCTCGCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1410

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
Db       1411 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1470

          1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
Db       1471 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1530

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
Db       1531 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1590

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
Db       1591 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACTACATCTTC 1650

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
Db       1651 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1710

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680
Db       1711 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 1746
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RESULT 14
AAQ28118
ID AAQ28118 standard; cDNA; 1983 BP.

XX
AC AAQ28118;
XX
DT 15-MAR-1993 (first entry)
XX
DE Human norepinepherine transporter protein cDNA clone.
XX
KW NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1914
FT /*tag= a
XX
PN WO9217568-A.
XX
PD 15-OCT-1992.
XX
PF 20-FEB-1992; 92WO-US01376.
XX
PR 28-MAR-1991; 91US-0676980.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Amara SG, Blakely RD, Pacholczyk T;
XX
DR WPI; 1992-366242/44.
DR P-PSDB; AAR26416.
XX
PT Complementary DNA clone encoding human norepinephrine transporter
PT protein - isolated from human neuroblastoma cells and useful for
PT determining action of e.g. antidepressant drugs
XX
PS Claim 3; Fig 1; 37pp; English.
XX
CC Pools of clones from a human SK-N-SH cell (a human neuroblastoma
CC cell line) cDNA library were transfected into COS-1 cells. The
CC transfected clones were in the form of expression vectors (pXM)
CC having an SV-40 replication origin to enable amplification.
CC Transfectants of these cells expressing the norepinepherine
CC transporter were identified by employing an assay exploiting the
CC fact that the norepinepherine analogue m-iodobenzylguanidine (m-IBG)
CC is accumulated intracellularly by SK-N-SH cells expressing the
CC intact NT. The accumulated radiolabelled m-IBG allows direct
CC autoradiographic visualisation of transporter expressing
CC transfectants. DNA was rescued from positive colonies and the
CC resulting plasmid pools rescreened and subdivided until a single
CC clone was obtd. Transfected cells become capable of norepinepherine
CC uptake, which may be inhibited by various drugs, e.g. cocaine, to
CC a degree similar to the effect of such drugs on noradrenergic
CC neurons. The cloned cDNA makes possible well-controlled studies
CC of neurotransmitter transporter function in non-neuronal cells
CC without the abfuscating influence of other transporters in the
CC same cell. Such studies include the relative effects of various
CC (psychotropic) drugs such as antidepressants.
XX
SQ Sequence 1983 BP; 384 A; 602 C; 529 G; 468 T; 0 other;

Query Match 29.6%; Score 522.4; DB 13; Length 1983;
Best Local Similarity 59.9%; Pred. No. 3.9e-131;
Matches 956; Conservative 0; Mismatches 616; Indels 24; Gaps 4;

```
Qy        103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
Db        217 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 276

Qy        163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
Db        277 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 336

Qy        223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
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Db        337 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 396

Qy        283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342

Db        397 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 453

Qy        343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402

Db        454 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 513

Qy        403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC------------TCTC 450

Db        514 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 573

Qy        451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509

Db        574 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 633

          510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564

Db        634 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 693

Qy        565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624

Db        694 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 753

Qy        625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684

Db        754 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 813

Qy        685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744

Db        814 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 873

Qy        745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804

Db        874 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 933

Qy        805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864

Db        934 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 993

Qy        865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924

Db        994 GCAACTCAGATATTTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 1053

          925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984

Db       1054 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1113

Qy        985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044

Db       1114 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1173

Qy       1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104

Db       1174 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1233

Qy       1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164

Db       1234 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1293

Qy       1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224

Db       1294 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1353

Qy       1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284

Db       1354 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1410

Qy       1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344

Db       1411 TTCAGCACTTTCCTTCTCGCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1470

Qy       1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404

Db       1471 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1530

Qy       1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464

Db       1531 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1590

Qy       1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524

Db       1591 TTCAAGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1650

Qy       1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584

Db       1651 TTCGTGGTTGTGGTCAGCATCATCAACTTCAAGCCACTCACCTACGACGACTACATCTTC 1710

Qy       1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644

Db       1711 CCGCCCTGGGCCAACTGGGTGGGGTGGGGCATCGCCCTGTCCTCCATGGTCCTGGTGCCC 1770

Qy       1645 CTTTACATTATCTACAAACTGCTCATCACTCCTGGC 1680

Db       1771 ATCTACGTCATCTATAAGTTCCTCAGCACGCAGGGC 1806
```

RESULT 15
AAH28083
ID AAH28083 standard; cDNA; 1854 BP.
XX
AC AAH28083;
XX
DT 05-SEP-2001 (first entry)
XX
DE DNA encoding human norepinephrine transporter variant A457P.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1..1854
FT   /*tag= a
FT   /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
DR P-PSDB; AAB84533.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene
XX
PS Claim 43; Page 104-108; 133pp; English.
XX
CC The present sequence encodes a variant norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises

CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;

Query Match 29.5%; Score 520.8; DB 22; Length 1854;
Best Local Similarity 59.8%; Pred. No. 1e-130;
Matches 955; Conservative 0; Mismatches 617; Indels 24; Gaps 4;

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Qy       103 GCGCGGCAGCGCGAGACCTGGGCGAAGAAGGCAGAGTTCCTGCTGGCGGTGGTGGGATTC 162
            |||| ||  || |||||||||  ||||||   || |||||||||| | || || || |||
Db       157 GCGCAGCCCCGGGAGACCTGGGGCAAGAAGATCGACTTCCTGCTGTCCGTAGTCGGCTTC 216

Qy       163 GCAGTGGATCTTGGTAACGTGTGGCGATTCCCCTACATCTGTTACCAGAATGGAGGCGGT 222
            |||||||| || |  |||||||||||| |||||||||| |||| ||| |||| || |||||
Db       217 GCAGTGGACCTGGCCAACGTGTGGCGCTTCCCCTACCTCTGCTACAAGAACGGCGGCGGT 276

Qy       223 GCGTTCCTGATCCCGTACTGCGTTATGCTGCTGTTTGGCGGGCTGCCGCTGTTCTTCCTG 282
            || ||| ||||||||||||    | | ||  |  | |  ||| |||| ||||||| | ||
Db       277 GCCTTCTTGATCCCGTACACACTGTTCCTTATCATCGCGGGGATGCCCCTGTTCTACATG 336

Qy       283 GAACTGGCGCTGGGCCAGTACCACCGCTGCGGCTGCCTCACTCTCTGGAAACGGATCTGC 342
            || ||||| ||||| ||||||| ||||    ||      |||  | ||||||   |||||| 
Db       337 GAGCTGGCTCTGGGACAGTACAACCGGGAGGGGGCTGCCACCGTTTGGAAA---ATCTGC 393

Qy       343 CCCGCGCTTAAAGGTGTCGGCTATGCCATCTGCATGATCGACATCTACATGGGCATGTAC 402
            ||     | ||||| || ||||||||  ||  | ||||||  | | ||| | ||| | |||
Db       394 CCATTCTTCAAAGGCGTTGGCTATGCTGTCATCCTGATCGCCCTGTACGTTGGCTTCTAC 453

Qy       403 TACAACACGATCATCGGATGGGCGGTGTATTACCTGATCGCTTC------------TCTC 450
            ||||||   |||||||  ||| |  | || |||||  || | ||            ||
Db       454 TACAACGTCATCATCGCCTGGTCACTCTACTACCTCTTCTCCTCCTTCACCCTCAACCTG 513

Qy       451 GCGTCTATAAACTCTGTGCTGCCATGGACCAGCTGCGACAACGAGTGGAACACGCCGCT- 509
             | |  |   ||| || |   | |||| ||||  | ||           || ||  ||
Db       514 CCCTGGACCGACTGTGGCCACACCTGGAACAGCCCCAACTGTACCGACCCCAAGCTCCTC 573

Qy       510 -----GTGCACGCCGGTCACCTCACCTCAGACTAATCCTAACTCTTCTACACCGGCGAAG 564
                 | |  ||  | || |    |  ||          ||   |  || |||||
Db       574 AATGGCTCCGTGCTTGGCAACCACACCAAGTACTCCAAGTACAAGTTCACGCCGGCAGCC 633

Qy       565 GAGTTCTTCGAACGTAATGTATTGGAGCAGCACAAGTCTAACGGCCTGGATGACATGGGG 624
            |||||  |  || |||  |||  || | |  ||| ||   | |||  |  |||||||  ||
Db       634 GAGTTTTATGAGCGTGGTGTCCTGCACCTTCACGAGAGCAGCGGGATTCATGACATCGGC 693

Qy       625 CCGATCAAGCCGTCGCTGGCTCTGTGTGTGTTCGGGGTCTTTGTCCTCGTCTACTTCTCC 684
             | |  |.||  |  |||    || ||| || | |  ||| |  || || | || ||   |
Db       694 CTGCCCCAGTGGCAGCTCTTGCTCTGTCTGATGGTCGTCGTCATCGTCTTGTATTTTAGC 753

Qy       685 TTGTGGAAAGGAGTCAGGAGTGCTGGCAAGGTGGTGTGGGTGACAGCTCTGGCCCCGTAC 744
             | |||||||| || | ||   | || ||||||||||||| | |||||   |   || |||
Db       754 CTCTGGAAAGGGGTGAAGACATCAGGAAAGGTGGTGTGGATCACAGCCACGCTGCCTTAC 813

Qy       745 GTGGTGCTGCTGATTCTGCTGGCGAGAGGCGTCACGCTTCCAGGAGCGACGGAGGGCATA 804
             | ||||||  |  | || ||||     |||||||||||| || |||||  |  | |||||
Db       814 TTCGTGCTGTTCGTGCTCCTGGTCCATGGCGTCACGCTGCCCGGAGCCTCCAATGGCATC 873

Qy       805 CGCTACTACCTTACCCCAGAGTGGCACAAATTGCAAAACTCTAAGGTATGGATTGACGCG 864
                 ||||||   |   || |   ||   ||| || |  | | ||||||||||| ||
Db       874 AATGCCTACCTGCACATCGACTTCTACCGCTTGAAAGAGGCCACGGTATGGATTGATGCC 933

Qy       865 GCATCCCAGATTTTCTTCTCGCTCGGTCCCGGGTTCGGAACCCTACTGGCGCTCTCCAGC 924
            ||| | ||||| || || ||  | ||  | || || |||    |  | ||  |  ||||
Db       934 GCAACTCAGATATTTTTTTCCTTGGGGGCTGGATTTGGAGTATTGATTGCATTTGCCAGT 993

Qy       925 TACAACAAGTTCAACAACAACTGCTACAGGGACGCGCTCATCACTTCTTCTATCAACTGC 984
             |||||||| ||  |||||||||| |||||||| || ||  | ||       ||||||||
Db       994 TACAACAAATTTGACAACAACTGTTACAGGGATGCCCTGCTGACCAGCAGCATCAACTGT 1053

Qy       985 TTGACCAGCTTCCTTGCTGGTTTCGTCATTTTCTCGGTTTTGGGGTACATGGCGCACGTT 1044
              | |||||||||  |  |||| |||| ||| |||||  |  | || |||||||| || |
Db      1054 ATCACCAGCTTCGTCTCTGGGTTCGCCATCTTCTCCATCCTTGGTTACATGGCCCATGAA 1113

Qy      1045 CAGAACAAGAGCATCGAGGAGGTTGGCCTCGAAGGCCCTGGACTGGTGTTCATCGTGTAC 1104
             || ||    | ||| ||||| || | |   |||||  |||| || |||||||||  ||||
Db      1114 CACAAGGTCAACATTGAGGATGTGGCCACAGAAGGAGCTGGCCTAGTGTTCATCCTGTAT 1173

Qy      1105 CCCGAGGCCATCGCCACCATGACCGGCTCCGTGTTCTGGGCCATCATCTTCTTCCTCATG 1164
             || |||||||  | ||| || | || ||    ||||||||  |  | || ||| |||||
Db      1174 CCAGAGGCCATTTCTACCCTGTCTGGATCTACATTCTGGGCTGTTGTGTTTTTCGTCATG 1233

Qy      1165 CTTATTACCCTGGGACTTGACAGTACTTTTGGAGGTCTTGAGGCAGTCACCACGGCTCTT 1224
             ||  |  | |||||  |||||||| |  | |||||  | |||||  |||| |||||  ||
Db      1234 CTCCTGGCGCTGGGCCTTGACAGCTCAATGGGAGGCATGGAGGCTGTCATCACGGGCCTG 1293

Qy      1225 TGCGACGAATATCCTCGAGTGTTAGGCAGACATCGCGAAGTATTTGTGGCTGTACTGCTT 1284
               || || |     |  ||  |      |||| ||  || | ||      ||   |
Db      1294 GCAGATGACT---TCCAGGTCCTGAAGCGACACCGGAAACTCTTCACATTTGGCGTCACC 1350

Qy      1285 CTGTTCATCTATATTTGCGCTCTGCCCACCACCACATACGGTGGTGTATACCTCGTAGAC 1344
              |  ||  |  ||  | | |||  |  ||  ||  | |||||  | ||| || |   |
Db      1351 TTCAGCACTTTCCTTCTCCCCCTGTTCTGCATAACCAAGGGTGGAATTTACGTCTTGACC 1410

Qy      1345 CTACTCAATGTGTATGGCCCTGGATTGGCGATTCTATTCGTGGTATTTGCTGAGGCTGCC 1404
             || ||  |    | ||   | ||      | || || || |  ||  |    || ||  |
Db      1411 CTCCTGGACACCTTTGCTGCGGGCACCTCCATCCTTTTTGCTGTCCTCATGGAAGCCATC 1470

Qy      1405 GGCGTGTGCTGGGTGTATGGCGTCGACCGGTTCTCTGAAGATGTGAGGACCATGCTGGGG 1464
             || || | |||| | ||||| || ||| |||||    | ||  |   |   ||| |||||
Db      1471 GGAGTTTCCTGGTTTTATGGAGTGGACAGGTTCAGCAACGACATCCAGCAGATGATGGGG 1530

Qy      1465 CACACCCCTGGATGGTTCTGGAGGACCTGTTGGTCTTACATCAGTCCCGTATTCTTGCTG 1524
               ||  || ||    | ||||||    || |||   | | ||||||| |  ||| | |||
Db      1531 TTCAGGCCGGGTCTATACTGGAGACTGTGCTGGAAGTTCGTCAGTCCTGCCTTCCTCCTG 1590

Qy      1525 GTGCTGTTCGTGTTCTCCGTTCTGGCACACGAGGAGATGCTCGGCGGGGAATACACCTAT 1584
              | || | ||| ||  | |  |     | ||    |   |  ||  || |||| ||
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Qy      1585 CCCTCATGGTCTATCACCGTAGGCTGGGTGATGACCGGCACCACCGTCTCGTGCATTCCT 1644
             ||  | ||| | | |   || || ||||  ||  ||    || || |         | ||
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Search completed: July 18, 2003, 15:24:19
Job time : 326 secs